Please amend the title of Table 13 at page 70, as follows:

a6 Table 13. Neurospora crassa UVDE Homolog (Genbank Accession No. BAA-74539) SEQ ID NO:36)

In the Claims

Please cancel claims 1-15 without prejudice.

Please amend claims 16-20 as follows:

16. (Once amended) A method for cleavage of a double-stranded DNA molecule characterized by a distorted structure, wherein said distorted structure results from ultraviolet radiation damage, a photoproduct, an abasic site, mismatched nucleotide pairing, a platinum diadduct, an intercalated molecule, an insertion deletion loop of five or fewer nucleotides or alkylation of a nucleotide or a uracil residue resulting from deamination of a cytosine residue, said method comprising the step of contacting a DNA molecule characterized by a distorted structure with a broadly specific DNA damage endonuclease selected from the group of endonucleases selected from the group consisting of an endonuclease identified by the amino acid sequence given in SEQ ID NO:2 wherein said endonuclease is purified, amino acids 230 to 828; a truncated stable truncated Uve1p identified by the amino acid sequence given in SEQ ID NO:4; the endonuclease identified by the amino acid sequence given in SEQ ID NO:36; the endonuclease identified by the amino acid sequence given in SEQ ID NO:37; the endonuclease identified by the amino acid sequence given in SEQ ID NO:38; the endonuclease identified by the amino acid sequence given in SEQ ID NO:39, under conditions allowing for enzymatic activity of said endonuclease and wherein the double stranded DNA molecule is not an oligonucleotide which has been irradiated with ultraviolet light or a closed circle plasmid DNA molecule which has been irradiated with ultraviolet light when the endonuclease is identified by the amino acid sequence of SEQ ID NO:36.

a7

17. (Once amended) The method of claim 16 wherein said truncated Uve1p has an amino acid sequence as given in SEQ ID NO:4.

18. (Once amended) A method for cleavage of a double-stranded DNA molecule characterized by a distorted structure, wherein said distorted structure results from ultraviolet radiation damage, a photoproduct, an abasic site, mismatched nucleotide pairing, a platinum diadduct, an insertion deletion loop, alkylation of a nucleotide, the presence of a uracil residue resulting from deamination of a cytosine residue, said method comprising the step of contacting a DNA molecule characterized by a distorted structure with a broadly specific DNA damage endonuclease selected from the group of endonucleases selected from the group consisting of an endonuclease consisting of the amino acid sequence given in SEQ ID NO:2, amino acids 230 to 828 wherein said endonuclease is purified; an endonuclease consisting of the sequence given in SEQ ID NO:6, a truncated stable truncated Uve1p identified by the amino acid sequence given in SEQ ID NO:4; the endonuclease identified by the amino acid sequence given in SEQ ID NO:36; the endonuclease identified by the amino acid sequence given in SEQ ID NO:37; the endonuclease identified by the amino acid sequence given in SEQ ID NO:38; the endonuclease identified by the amino acid sequence given in SEQ ID NO:39, under conditions allowing for enzymatic activity of said endonuclease.

a7 cont

19. (Once amended) The method of claim 18 wherein said truncated Uve1p has an amino acid sequence as given in SEQ ID NO:4.

20. (Once amended) The method of claim 16 wherein the insertion deletion loop is of four or fewer nucleotides.

add B2

REMARKS

Claims 1-15 have been canceled without prejudice, pursuant to the issue of the U.S. Patent No. 6,368,594 B1 (from which the present application claims priority) and the restriction